

Figure 1. Sequence of full length C1 (ILKAP) and C1 clone.

```

1 ggcaccaggcccgctgctgcccgcgggggtgtggagcccgccgctgctgcgggctgagtgctgtcgtgctgcccgcctccaccagcctccgc 100
101 c ATG GAC CTC TTC GGG GAC CTG CCG GAG CCC GAG CGC TCG CCG CGC CCG GCT GCC GGG AAA GAA GCT CAG AAA 173
1 M D L F G D L P E P E R S P R P A A G K E A Q K 24
174 GGA CCC CTG CTC TTT GAT GAC CTC CCT CCG GCC AGC AGT ACT GAC TCA GGA TCA GGG GGA CCT TTG CTT TTT GAT 248
25 G F L L F D D L P P A S S T D S G S G G P L L F D 49
249 GAT CTC CCA CCC GCT AGC AGT GGC GAT TCA GGT TCT CTT GCC ACA TCA ATA TCC CAG ATG GTA AAG ACT GAA GGG 323
50 D L P P A S S G D S G S L A T S I S Q M V K T E G 74
324 AAA GGA GCA AAG AGA AAA ACC TCC GAG GAA GAG AAG AAT GGC AGT GAA GAG CTT GTG GAA AAG AAA GTT TGT AAA 398
75 K G A K R K T S E E E K N G S E E L V E K K V C K 99
399 GCC TCT TCG GTG ATC TTT GGT CTG AAG GGC TAT GTG GCT GAG CGG AAG GGT GAG AGG GAG GAG ATG CAG GAT GCC 473
100 A S S V I F G L K G Y V A E R K G E R E E M Q D A 124
474 CAC GTC ATC CTG AAC GAC ATC ACC GAG GAG TGT AGG CCC CCA TCG TCC CTC ATT ACT CGG GTT TCA TAT TTT GCT 548
125 H V I L N D I T E E C R P P S S L I T R V S Y F A 149
549 GTT TTT GAT GGA CAT GGA GGA ATT CGA GCC TCA AAA TTT GCT GCA CAG AAT TTG CAT CAA AAC TTA ATC AGA AAA 623
150 V F D G H G G I R A S K F A A Q N L H Q N L I R K 174
624 TTT CCT AAA GGA GAT GTA ATC AGT GTA GAG AAA ACC GTG AAG AGA TGC CTT TTG GAC ACT TTC AAG CAT ACT GAT 698
175 F P K G D V I S V E K T V K R C L D T F K H T D 199
699 GAA GAG TTC CTT AAA CAA GCT TCC AGC CAG AAG CCT GCC TGG AAA GAT GGG TCC ACT GCC ACG TGT GTT CTG GCT 773
200 E E F L K Q A S S Q K P A W K D G S T A T C V L A 224
774 GTA GAC AAC ATT CTT TAT ATT GCC AAC CTC GGA GAT AGT CGG GCA ATC TTG TGT CGT TAT AAT GAG GAG AGT CAA 848
225 V D N I L Y I A N L G D S R A I L C R Y N E E S Q 249
849 AAA CAT GCA GCC TTA AGC CTC AGC AAA GAG CAT AAT CCA ACT CAG TAT GAA GAG CGG ATG AGG ATA CAG AAG GCT 923
250 K A A A L S K E H N P T Q Y E E R M R I Q K A 274
924 GGA GGA AAC GTC AGG GAT GGG CGT GTT TTG GGC GTG CTA GAG GTG TCA CGC TCC ATT GGG GAC GGG CAG TAC AAG 998

275 G G N V R D G R V L G V L E V S R S I G D G Q Y K 299
999 CGC TGC GGT GTC ACC TCT GTG CCC GAC ATC AGA CGC TGC CAG CTG ACC CCC AAT GAC AGG TTC ATT TTG TTG GCC 1073
300 R C G V T S V P D I R R C Q L T P N D R F I L L A 324
1074 TGT GAT GGG CTC TTC AAG GTC TTT ACC CCA GAA GAA GCC GTG AAC TTC ATC TTG TCC TGT CTC GAG GAT GAA AAG 1148
325 C D G L F K V F T P E E A V N F I L S C L E D E K 349
1149 ATC CAG ACC CGG GAA GGG AAG TCC GCA GCC GAC GCC CGC TAC GAA GCA GCC TGC AAC AGG CTG GCC AAC AAG GCG 1223
350 I Q T R E G K S A A D A R Y E A A C N R L A N K A 374
1224 GTG CAG CGG GGC TCG GCC GAC AAC GTC ACT CTG ATG GTG GTG CGG ATA GGG CAC TGA ggggtggcgccggccaggagcac 1304
375 V Q R G S A D N V T V M V V R I G H * 393
1305 gcatggtattgactttaaagggttcattttgtgtgtgtgcacattgtgtttttgtgtactcctgtgggactcccatggttgaataaagggtttctcttt 1404
1405 ttttccctaaaaaaaaa 1422

```

0955124-002107